

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
Q9QYX7	PCLO_MOUSE	Mus musculus	Protein piccolo	69.559855	S518;S717;S723;T733;S2268;S2314;T2315;T2382;T2386;T2394;T2455;S2473;S2476;T2481;S2626;S2664;T2669;T2686;T2717;T2836;T2839;S2845;S2881;T2883;T2889;T2890;S2924;T2948;S2960;S2969;T2971;T2972;T2978;S2983;S2988;S2993;S3048;T3052;T3053;S3058;T3770;T3903;S3904;S3920;T3921;S3956;S3991;S4212;S4313;S4584	S212;S844;S856;T860;T1120;S1292;S1302;S1303;S1332;S1334;S1337;S1338;S1341;S1439;S1451;S1452;S1454;S1457;S1481;S1484;S1505;S1507;T1552;S1553;S1563;S1575;S1638;T1640;S1642;S1647;S1708;S1709;T1760;S1766;S1795;S1800;S1808;S1829;S2495;T2998;S3358;S3372;T3376;T3403;S3506;S3514;S3545;S3549;S3555;S3558;S3561;S3582;S3608;S3610;S3616;S3763;S4016;S4042;S4132;S4286;S4290;S4293;S4322;S4358;S4592;S4706	22826440;19458039;22645316;36757814;26192747;22517741;33300544;34678516;16452088;35822049	MGNEASLEGEGLPEGLAAAAGGAG GSGSALHPGIPAGMEADLSQLSEEE RRQIAAVMSRAOGLPKGSVPA AAAE SPSMHRKQELDSSQAPQPGKPPDP GRPPQHGLSKSRITDFFRSEQKLPG RSPSTISLKESKSRITDFKEEYKSSMM PGFFSDVNPLSAVSSVNVKNFNFDFLI SDSEAVQEETTKKQKVAQKQDGKSE GITKPSLQOPSPKLPKQGGPGKEVIP QDIPSKSVSSQQAETKQPAPGTAKP SQQSPAQTPAQQAQKPAVQPGPAKA TVQQPGPAKSPAQAGTGKSPAQPP VTAKPPAQAGLEKTSLQOPGPKSL AQTPGGQKVPPGPAKSPAQPGTAK LPAQQPGPOTAAKVPGPTKTTPAQLS GPGKTPAQPGPTKPSPOPIPAKPQ PQQPVATKPPQPPAPAKPQPHPT PAKPQPHPTPAKPQPPQPTPAKPQ PQQPTPAKPQPPQPTPAKPQPHPT PAKPQPPQGLGKPSAQGPSKISOT VTGRPLQAPPTSAQAQAQGLSKTIC PLCNTTELLHTPEKANFNCTECQ STVCSLCGFNPNPHLTHEIKEWLCLN CQMORALGGELAAIPSSPOPTKAA SVQPATASKSPVPSQQASPKKELPSK QDSPKAPESKKPPPLVQPTLHGPTP ATAPQPPVAEALPKPAPPKPSAALP EQAKAPVADVEPKQPKTTTETLDS SAAATSKPAILSSVQQAQVTTAPP LKTDSAKTSQSFPTGDTITPLDSKA MPRPASDSKIVSHPGPTSESKDPVQ KKEEPKKAQTKVTPKPDTKVPKGVSP TPSGTRPTTGGQATPQSQPPKPEQS RRFSLNLGGIADAPKSOPTTPOETVT GKLFGFASIFSOASNLISITAGQOAP HPQTGPAAPSKQAPPSSQTLAAQGP PKSTGPHPSAPAKTTAVKKETKGPAA ENLEAKPVQAPTVKKAEDKKPPPG KVSKPPTEPEKAVLAQKPKDKTTKPK PACPLCRTELNVGSDPPNFNTCTE CKNQVCNLCGFNPTPHLTHEIQEWLC LNCOTQRAISGQLGDMDKMPASS GPKASVPAPAEPPPKTPTAAHAKG KKKETE VKAETE KQIPEKETPSIEKT PPAVATDQKLEESVTKSLVSVLPEK KPEEEKALPADKKEKPPAAEAPPL EEKKPIPDDQKLPPDAKPSASEGEEK RDLKKAHVQIPEEGPIGKVASLACEG EQQPDTRPEDLPGATPOTLPKDRQK ESRDVTQPAEGTAKEGRGEPKSKDR TEKEEDKSDTSSSQPKSPQGLSDT GYSSDGISGSLGEIPSLIPSEKDLLK GLKKDSFSQESSPSSPSDLAKLESTV LSILEAAQSTLVGEKAEKKTQPKQVS PEQPQDQKTQTPSETRDISISEEEI KESQEKKVTSKKDSAQGFPSRKEHK ENPELVDDLSPRRASYDSVEDSSES ENSPVARRKRRTSIGSSSEYKQED SQGSGEDED FIRKQIHEMSADEDASG SEDEEFIRSQKKEIGGVTESQKREET KGGKSPAGKHRRLTRKSSSFDDDD AGRRHSWHDEDETTFDESPELKFR ETKSQESEELVAGGGLLRRFKTIEL NSTVIDKYSAESSQKKTLYFDEEPE LEMESLTDSPEDRSRGE GSSSLHAS SFTPGTSPTSVSSLDESDSSPSHKK GESKQQRKARHRSHGPLLPTIEDSS EEEELREEEELKQEQKQRELEQQQ RKSSSKSKKDKDELRAQRREPK TPPSNLSPIEDASPTTELRAAEMEE LHRSSCSSEYSPSIESDPEGFEISPEKI IEVQKVYKLP TAVSLYPTDEQSVMQ KEGAQKALSAEEMYEEMMHKPHK YKAFPAANERDEVFEKEPLYGGMLI EDYIYESLVEDTYNGSVDGSLLTRQD EQNGFMQQRGREQKIRLQEQIYDDP MQKITDLQKEFYELESLSHIVPQEDI VSSSYIIPESHEIVDLGSMVTSSEEK KLLDADAAYEELMKRQMQVTDGGS SLIQTMMGDDMAESTLDFDRVQDAS	None	None	None	None	None

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 QHFSTEEFEDEYVTDYTRIEQEHIAH
 ESLILTYSEPSSEATSVPSPDTPSLTS
 SSSVCTDSSSPVTTLDLSTTVYTEP
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